

# Fine Scale Tools and Limiting Factor Analysis

December 7, 2006

# Steelhead White Paper - Management Plan Implementation Steps

- Steelhead White Paper Recommendation
- Coarse Filter
  - identifies watersheds to conduct gene flow and other analyses
- Gene Flow Analysis (or other analyses)
  - estimates range of potential gene flow
- Limiting Factor Analysis
  - identifies constraints on achieving population VSP
  - evaluates alternative approaches to address constraints
- Watershed Management Plan documents:
  - analysis
  - decision
  - adaptive management approach

# Draft Steelhead White Paper

***Finding 3-4.*** Chambers Creek Winter and Skamania River Summer steelhead pose a high potential genetic risk.

***Recommendation 3-1.*** Evaluate the potential range of gene flow from returning adults to natural populations in all watersheds where Chambers Winter, Skamania Summer, or other nonlocal steelhead are released. Where risks are inconsistent with policy objectives for the natural population, implement one or more of the following actions...

# What are Concerns?

- Domestication - loss of productivity
- Loss of among population diversity

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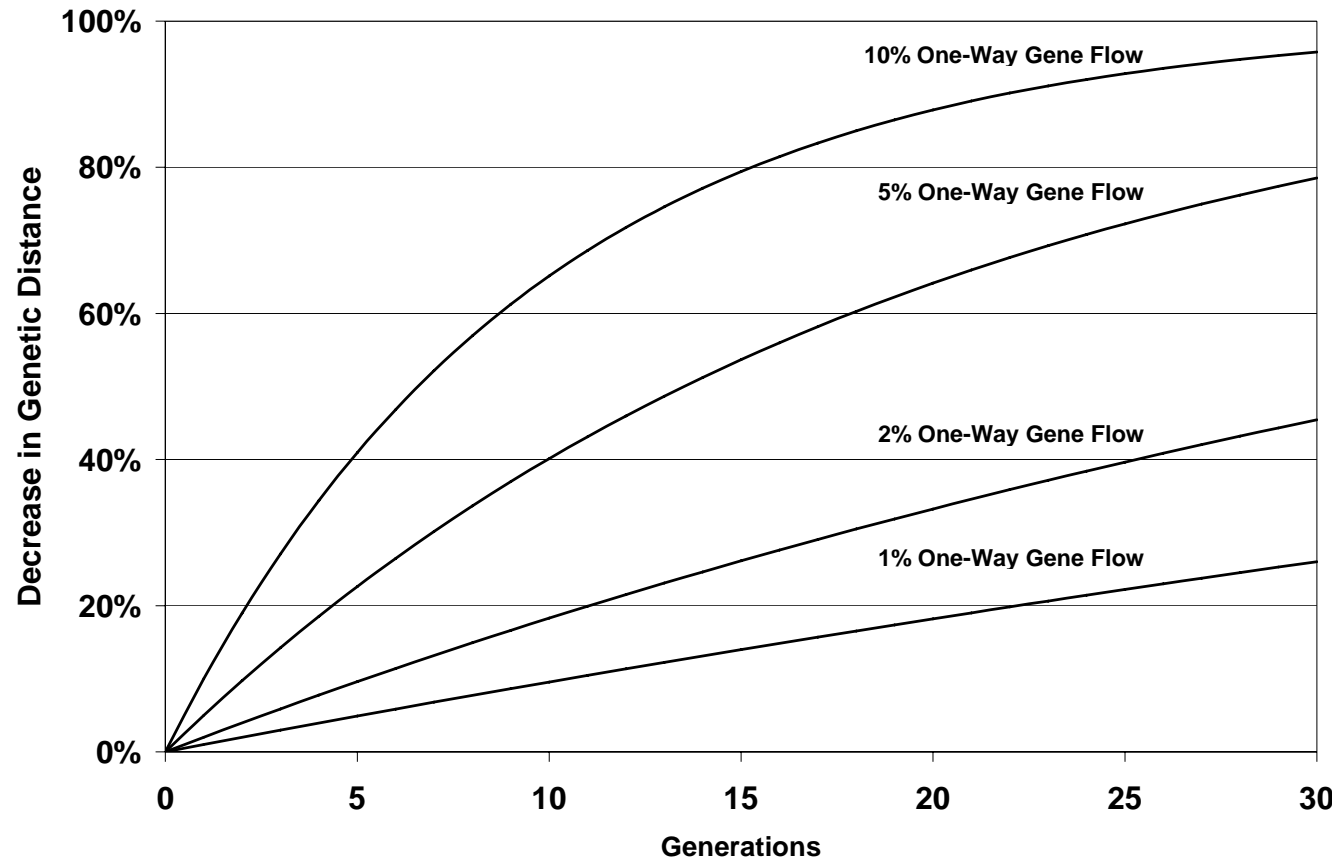


Figure 3-8. Decay of selectively neutral genetic differences between a donor and recipient population under varying levels of one-way gene flow.

# Gene Flow Analysis

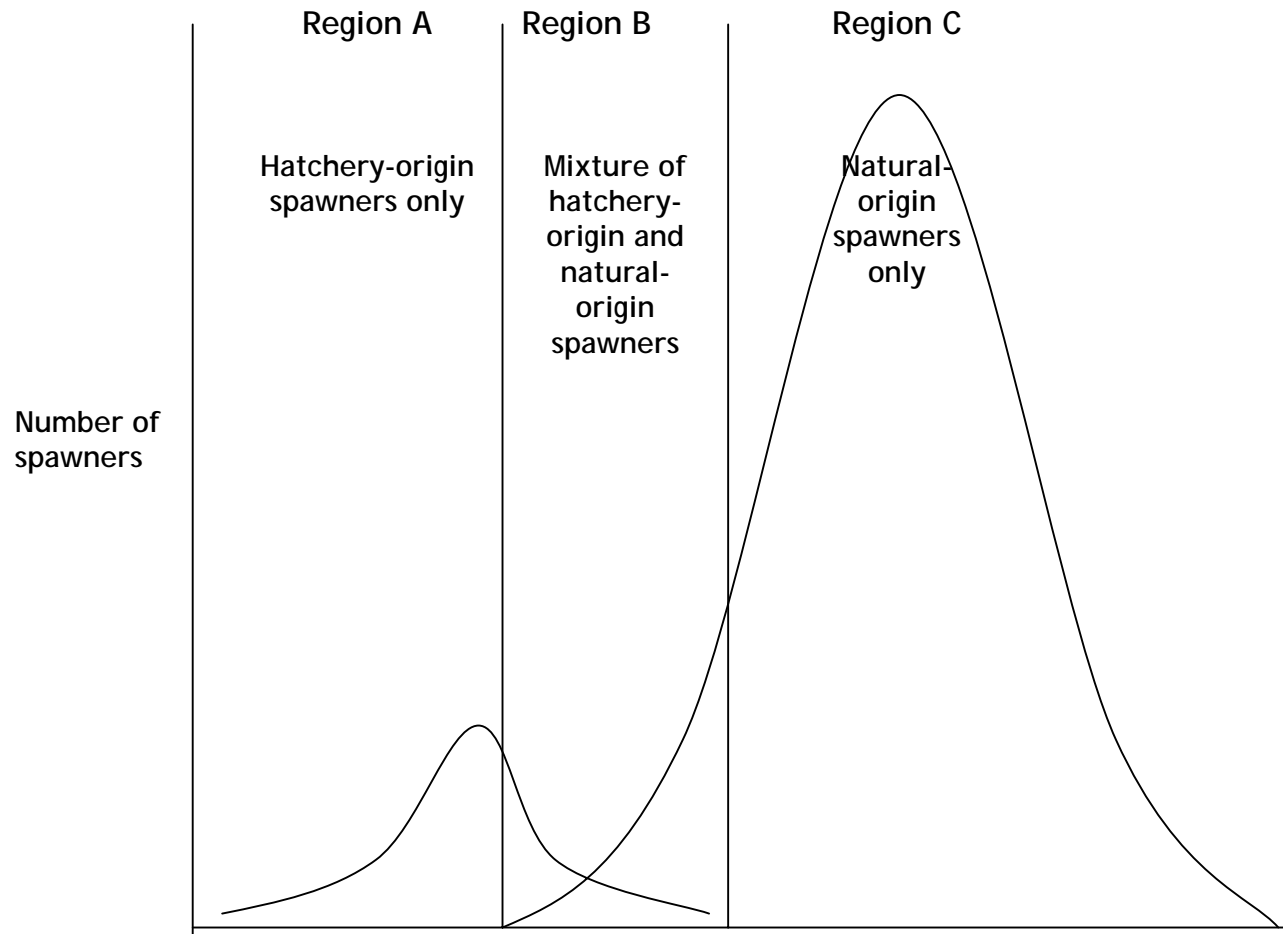


Figure 3-7. Schematic of temporal spawning overlap between early-run hatchery-origin winter steelhead and natural-origin winter steelhead. The shape, sizes, and placement of curves does not represent any particular real situation.

# Gene Flow Analysis

- Information Requirements
  - Number of hatchery-origin spawners
  - Spawn timing of hatchery-origin spawners
  - Spawning location of hatchery-origin spawners
  - Relative reproductive success of hatchery-origin spawners
  - Number of natural-origin spawners
  - Spawn timing of natural-origin spawners
  - Spawning location of natural-origin spawners

# Gene Flow Analysis

## A. Preferred and alternative data sources for hatchery-origin spawners

Data Type	Preferred Data	Alternative Data Source
Number of Natural Spawners	Watershed specific estimated number of spawners.	a) Watershed specific estimates of survival rate and harvest rate. b) Average survival rate and harvest rate.
Spawn Timing	Watershed specific estimate of spawn timing.	a) Average spawn timing in other watersheds. b) Average spawn timing in hatcheries.
Spawning Location	Watershed specific estimate of spawning location.	Assume same location as natural-origin spawners.
Relative Reproductive Success	Watershed specific estimate of relative reproductive success.	Average reproductive success in other watersheds.

## B. Preferred and alternative data sources for natural-origin spawners

Data Type	Preferred Data	Alternative Data Source
Number of Natural Spawners	Watershed specific estimated number of spawners.	
Spawn Timing	Watershed specific estimate of spawn timing.	Average spawn timing in other ecologically similar watersheds.

# Gene Flow Analysis

Draft Steelhead White Paper, page 3-25

$$\text{Gene flow} = \frac{b}{b + a(1 - q)(1 - o_N) + (1 - q)^2 o_N^2}, \text{ where}$$

$$a = o_N + q(o_H - o_N)$$

$$b = k_1(aq(1 - o_H) + q^2 o_H^2) + k_2 q(1 - q)o_N o_H$$

where:

$k_1$  and  $k_2$  are the fitnesses of HxH and HxN matings relative to NxN, respectively;  
 $q$  is the proportion of hatchery fish among all spawners (regardless of overlap);  
 $o_h$  is the proportion of the hatchery spawners that are in the overlap region;  
 $o_n$  is the proportion of the natural-origin spawners that are in the overlap region